

10/578614

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SEQUENCE LISTING

<110> Toyota Central R&D Labs., Inc.
Toyota Jidosha Kabushiki Kaisha

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<150> JP2003-379076

<151> 2003-11-07

<160> 47

<170> PatentIn version 3.1

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<222> (1).. (999)

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His Val Pro Gln Asn Lys Ile Thr Ile Val Gly Val Gly Ala Val Gly	
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atg gcc tgt gcc atc agt atc tta atg aag gac ttg gca gat gaa gtt	144
Met Ala Cys Ala Ile Ser Ile Leu Met Lys Asp Leu Ala Asp Glu Val	
35 40 45	
gct ctt gtt gat gtc atg gaa gat aaa ctg aag gga gag atg atg gat	192
Ala Leu Val Asp Val Met Glu Asp Lys Leu Lys Gly Glu Met Met Asp	
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ctc caa cat ggc agc ctt ttc ctt aga aca cca aaa att gtc tct ggc	240
Leu Gln His Gly Ser Leu Phe Leu Arg Thr Pro Lys Ile Val Ser Gly	
65 70 75 80	
aaa gac tat aat gtg aca gca aac tcc agg ctg gtt att atc aca gct	288
Lys Asp Tyr Asn Val Thr Ala Asn Ser Arg Leu Val Ile Ile Thr Ala	
85 90 95	
ggg gca cgt cag caa gag gga gag agc cgt ctg aat ttg gtc cag cgt	336
Gly Ala Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln Arg	
100 105 110	
aac gtg aac atc ttt aaa ttc atc att cct aat att gta aaa tac agc	384
Asn Val Asn Ile Phe Lys Phe Ile Ile Pro Asn Ile Val Lys Tyr Ser	
115 120 125	
cca aat tgc aag ttg ctt gtt gtt tcc aat cca gtc gat att ttg acc	432
Pro Asn Cys Lys Leu Leu Val Val Ser Asn Pro Val Asp Ile Leu Thr	
130 135 140	
tat gtg gct tgg aag ata agt ggc ttt ccc aaa aac cgt gtt att gga	480
Tyr Val Ala Trp Lys Ile Ser Gly Phe Pro Lys Asn Arg Val Ile Gly	
145 150 155 160	

agt ggt tgc aat ctg gat tca gct cgc ttc cgt tat ctc atg ggg gag	528
Ser Gly Cys Asn Leu Asp Ser Ala Arg Phe Arg Tyr Leu Met Gly Glu	
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Arg Leu Gly Val His Pro Leu Ser Cys His Gly Trp Ile Leu Gly Glu	
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His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Val Ala Gly	
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Val Ser Leu Lys Asn Leu His Pro Glu Leu Gly Thr Asp Ala Asp Lys	
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gaa cag tgg aaa gcg gtt cac aaa caa gtg gtt gac agt gct tat gag	720
Glu Gln Trp Lys Ala Val His Lys Gln Val Val Asp Ser Ala Tyr Glu	
225 230 235 240	
gtg atc aaa ctg aaa ggc tac aca tcc tgg gcc att gga ctg tca gtg	768
Val Ile Lys Leu Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val	
245 250 255	
gcc gat ttg gca gaa agt ata atg aag aat ctt agg cgg gtg cat ccg	816
Ala Asp Leu Ala Glu Ser Ile Met Lys Asn Leu Arg Arg Val His Pro	
260 265 270	
att tcc acc atg att aag ggt ctc tat gga ata aaa gag gat gtc ttc	864
Ile Ser Thr Met Ile Lys Gly Leu Tyr Gly Ile Lys Glu Asp Val Phe	
275 280 285	
ctt agt gtt cct tgc atc ttg gga cag aat gga atc tca gac gtt gtg	912
Leu Ser Val Pro Cys Ile Leu Gly Gln Asn Gly Ile Ser Asp Val Val	
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aaa gtg act ctg act cat gaa gaa gag gcc tgt ttg aag aag agt gca	960
Lys Val Thr Leu Thr His Glu Glu Glu Ala Cys Leu Lys Lys Ser Ala	
305 310 315 320	
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 35 40 45

Ala Leu Val Asp Val Met Glu Asp Lys Leu Lys Gly Glu Met Met Asp
 50 55 60

Leu Gln His Gly Ser Leu Phe Leu Arg Thr Pro Lys Ile Val Ser Gly
 65 70 75 80

Lys Asp Tyr Asn Val Thr Ala Asn Ser Arg Leu Val Ile Ile Thr Ala
 85 90 95

Gly Ala Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln Arg
 100 105 110

Asn Val Asn Ile Phe Lys Phe Ile Ile Pro Asn Ile Val Lys Tyr Ser
 115 120 125

Pro Asn Cys Lys Leu Leu Val Val Ser Asn Pro Val Asp Ile Leu Thr
 130 135 140

Tyr Val Ala Trp Lys Ile Ser Gly Phe Pro Lys Asn Arg Val Ile Gly
 145 150 155 160

Ser Gly Cys Asn Leu Asp Ser Ala Arg Phe Arg Tyr Leu Met Gly Glu
 165 170 175

Arg Leu Gly Val His Pro Leu Ser Cys His Gly Trp Ile Leu Gly Glu
 180 185 190

His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Val Ala Gly
 195 200 205

Val Ser Leu Lys Asn Leu His Pro Glu Leu Gly Thr Asp Ala Asp Lys
 210 215 220

Glu Gln Trp Lys Ala Val His Lys Gln Val Val Asp Ser Ala Tyr Glu
 225 230 235 240

Val Ile Lys Leu Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val
 245 250 255

Ala Asp Leu Ala Glu Ser Ile Met Lys Asn Leu Arg Arg Val His Pro
 260 265 270

Ile Ser Thr Met Ile Lys Gly Leu Tyr Gly Ile Lys Glu Asp Val Phe
 275 280 285

Leu Ser Val Pro Cys Ile Leu Gly Gln Asn Gly Ile Ser Asp Val Val
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 Met Ala Thr Leu Lys Asp Gln Leu Ile Gln Asn Leu Leu
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aaa gaa gaa cat gtt cca caa aat aaa att act att gtt ggt gtt ggt 99
 Lys Glu Glu His Val Pro Gln Asn Lys Ile Thr Ile Val Gly Val Gly
 15 20 25

gct gtt ggt atg gct tgt gct att tct att ttg atg aaa gat ttg gct 147
 Ala Val Gly Met Ala Cys Ala Ile Ser Ile Leu Met Lys Asp Leu Ala
 30 35 40 45

gat gaa gtt gct ttg gtt gat gtt atg gaa gat aaa ttg aaa ggt gaa 195

Asp	Glu	Val	Ala	Leu	Val	Asp	Val	Met	Glu	Asp	Lys	Leu	Lys	Gly	Glu		
				50					55					60			
atg	atg	gat	ttg	caa	cat	ggt	tct	ttg	ttt	ttg	aga	act	cca	aaa	att		243
Met	Met	Asp	Leu	Gln	His	Gly	Ser	Leu	Phe	Leu	Arg	Thr	Pro	Lys	Ile		
			65					70					75				
gtt	tct	ggt	aaa	gat	tat	aat	gtt	act	gct	aat	tct	aga	ttg	gtt	att		291
Val	Ser	Gly	Lys	Asp	Tyr	Asn	Val	Thr	Ala	Asn	Ser	Arg	Leu	Val	Ile		
		80					85					90					
att	act	gct	ggt	gct	aga	caa	caa	gaa	ggt	gaa	tct	aga	ttg	aat	ttg		339
Ile	Thr	Ala	Gly	Ala	Arg	Gln	Gln	Glu	Gly	Glu	Ser	Arg	Leu	Asn	Leu		
	95					100					105						
gtt	caa	aga	aat	gtt	aat	att	ttt	aaa	ttt	att	att	cca	aat	att	gtt		387
Val	Gln	Arg	Asn	Val	Asn	Ile	Phe	Lys	Phe	Ile	Ile	Pro	Asn	Ile	Val		
110					115					120					125		
aaa	tat	tct	cca	aat	tgt	aaa	ttg	ttg	gtt	gtt	tct	aat	cca	gtt	gat		435
Lys	Tyr	Ser	Pro	Asn	Cys	Lys	Leu	Leu	Val	Val	Ser	Asn	Pro	Val	Asp		
				130					135					140			
att	ttg	act	tat	gtt	gct	tgg	aaa	att	tct	ggt	ttt	cca	aaa	aat	aga		483
Ile	Leu	Thr	Tyr	Val	Ala	Trp	Lys	Ile	Ser	Gly	Phe	Pro	Lys	Asn	Arg		
			145					150					155				
gtt	att	ggt	tct	ggt	tgt	aat	ttg	gat	tct	gct	aga	ttt	aga	tat	ttg		531
Val	Ile	Gly	Ser	Gly	Cys	Asn	Leu	Asp	Ser	Ala	Arg	Phe	Arg	Tyr	Leu		
		160					165					170					
atg	ggt	gaa	aga	ttg	ggt	gtt	cat	cca	ttg	tct	tgt	cat	ggt	tgg	att		579
Met	Gly	Glu	Arg	Leu	Gly	Val	His	Pro	Leu	Ser	Cys	His	Gly	Trp	Ile		
	175					180					185						
ttg	ggt	gaa	cat	ggt	gat	tct	tct	gtt	cca	gtt	tgg	tct	ggt	gtt	aat		627
Leu	Gly	Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn		
190					195					200					205		
gtt	gct	ggt	gtt	tct	ttg	aaa	aat	ttg	cat	cca	gaa	ttg	ggt	act	gat		675
Val	Ala	Gly	Val	Ser	Leu	Lys	Asn	Leu	His	Pro	Glu	Leu	Gly	Thr	Asp		
				210					215					220			
gct	gat	aaa	gaa	caa	tgg	aaa	gct	gtt	cat	aaa	caa	gtt	gtt	gat	tct		723
Ala	Asp	Lys	Glu	Gln	Trp	Lys	Ala	Val	His	Lys	Gln	Val	Val	Asp	Ser		
			225					230					235				
gct	tat	gaa	gtt	att	aaa	ttg	aaa	ggt	tat	act	tct	tgg	gct	att	ggt		771
Ala	Tyr	Glu	Val	Ile	Lys	Leu	Lys	Gly	Tyr	Thr	Ser	Trp	Ala	Ile	Gly		

240	245	250	
ttg tct gtt gct gat ttg gct gaa tct att atg aaa aat ttg aga aga			819
Leu Ser Val Ala Asp Leu Ala Glu Ser Ile Met Lys Asn Leu Arg Arg			
255	260	265	
gtt cat cca att tct act atg att aaa ggt ttg tat ggt att aaa gaa			867
Val His Pro Ile Ser Thr Met Ile Lys Gly Leu Tyr Gly Ile Lys Glu			
270	275	280	285
gat gtt ttt ttg tct gtt cca tgt att ttg ggt caa aat ggt att tct			915
Asp Val Phe Leu Ser Val Pro Cys Ile Leu Gly Gln Asn Gly Ile Ser			
290	295	300	
gat gtt gtt aaa gtt act ttg act cat gaa gaa gaa gct tgt ttg aaa			963
Asp Val Val Lys Val Thr Leu Thr His Glu Glu Glu Ala Cys Leu Lys			
305	310	315	
aaa tct gct gat act ttg tgg ggt att caa aaa gaa ttg caa ttt taa			1011
Lys Ser Ala Asp Thr Leu Trp Gly Ile Gln Lys Glu Leu Gln Phe			
320	325	330	
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 <212> PRT
 <213> Artificial

<220>
 <223> synthetic DNA

<400> 43

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			20					25					30		

Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Met	Lys	Asp	Leu	Ala	Asp	Glu	Val
		35					40					45			

Ala	Leu	Val	Asp	Val	Met	Glu	Asp	Lys	Leu	Lys	Gly	Glu	Met	Met	Asp
50						55					60				

Leu Gln His Gly Ser Leu Phe Leu Arg Thr Pro Lys Ile Val Ser Gly
65 70 75 80

Lys Asp Tyr Asn Val Thr Ala Asn Ser Arg Leu Val Ile Ile Thr Ala
85 90 95

Gly Ala Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln Arg
100 105 110

Asn Val Asn Ile Phe Lys Phe Ile Ile Pro Asn Ile Val Lys Tyr Ser
115 120 125

Pro Asn Cys Lys Leu Leu Val Val Ser Asn Pro Val Asp Ile Leu Thr
130 135 140

Tyr Val Ala Trp Lys Ile Ser Gly Phe Pro Lys Asn Arg Val Ile Gly
145 150 155 160

Ser Gly Cys Asn Leu Asp Ser Ala Arg Phe Arg Tyr Leu Met Gly Glu
165 170 175

Arg Leu Gly Val His Pro Leu Ser Cys His Gly Trp Ile Leu Gly Glu
180 185 190

His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Val Ala Gly
195 200 205

Val Ser Leu Lys Asn Leu His Pro Glu Leu Gly Thr Asp Ala Asp Lys
210 215 220

Glu Gln Trp Lys Ala Val His Lys Gln Val Val Asp Ser Ala Tyr Glu
225 230 235 240

Val Ile Lys Leu Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val
245 250 255

Ala Asp Leu Ala Glu Ser Ile Met Lys Asn Leu Arg Arg Val His Pro
 260 265 270

Ile Ser Thr Met Ile Lys Gly Leu Tyr Gly Ile Lys Glu Asp Val Phe
 275 280 285

Leu Ser Val Pro Cys Ile Leu Gly Gln Asn Gly Ile Ser Asp Val Val
 290 295 300

Lys Val Thr Leu Thr His Glu Glu Glu Ala Cys Leu Lys Lys Ser Ala
 305 310 315 320

Asp Thr Leu Trp Gly Ile Gln Lys Glu Leu Gln Phe
 325 330

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 <213> Artificial

<220>
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34

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<212> DNA

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<223> synthetic primer

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31